Amendments to the specification

Please add the following new paragraph to the specification on page 1, line 26, after the first paragraph of priority claims and before "FIELD OF THE INVENTION".

The claimed invention, in the field of functional genomics and the characterization of plant genes for the improvement of plants, was made by or on behalf of Mendel Biotechnology, Inc. and Monsanto Corporation as a result of activities undertaken within the scope of a joint research agreement, said agreement having been in effect on or before the date the claimed invention was made.

Please replace the entire paragraph at page 9, lines 13-16 with the following amended paragraph:

CD-ROM1 is a read-only memory computer-readable compact disc and contains a copy of the Sequence Listing in ASCII text format. The Sequence Listing is named "MBI0034CIP.ST25.txt", was originally created on September 23, 2003, and is 153 kilobytes in size. The copies of the Sequence Listing on the CD-ROM disc are hereby incorporated by reference in their entirety.

Please replace the entire paragraph at page 25, lines 15-24 with the following amended paragraph:

In yet another example, Gilmour et al. (1998, Plant J. 16: 433-442) teach an *Arabidopsis* AP2 transcription factor, CBF1 (SEQ ID NO: 70), which, when overexpressed in transgenic plants, increases plant freezing tolerance. Jaglo et al. (2001, *Plant Physiol.* 127: 910-917) further identified sequences in *Brassica napus* which encode CBF-like genes and that transcripts for these genes accumulated rapidly in response to low temperature. Transcripts encoding CBF-like proteins were also found to accumulate rapidly in response to low temperature in wheat, as well as in tomato. An alignment of the CBF proteins from *Arabidopsis*, *B. napus*, wheat, rye, and tomato revealed the presence of conserved consecutive amino acid residues, PKK/RPAGRxKFxETRHP (SEQ ID NO: 79) and DSAWR (SEQ ID NO: 80), that bracket the AP2/EREBP DNA binding domains of the proteins and distinguish them from other members of the AP2/EREBP protein family. (See Jaglo et al. supra.)

Please replace the entire paragraph at page 26, lines 10-29 with the following amended paragraph:

In higher organisms, genomic DNA is assembled into multilevel complexes with a range of DNA-binding proteins, including the well-known histones and non-histone proteins such as the high mobility group (HMG) proteins. HMG proteins are classified into different groups based on their DNA-binding motifs, and one such group is the HMG-I(Y) subgroup (recently renamed as HMGA). Proteins in this group have been shown to bind to the minor groove of DNA via a conserved nine amino acid peptide (KRPRGRPKK; SEQ ID NO: 81) called the AT-hook motif (Reeves and Nisson (1995) *Biol. Chem.* 265:

8573-8582). At the center of this AT-hook motif is a short, strongly conserved tripeptide of glycine-arginine-proline (GRP). This simple AT-hook motif can be present in a variable number of copies (1-15) in a given AT-hook protein. For example, the mammalian HMGA1 protein has three copies of this motif. The mammalian HMGA proteins participate in a wide variety of nuclear processes ranging from chromosome and chromatin remodeling, to acting as architectural transcription factors that regulate the expression of numerous genes in vivo. As a result, these proteins influence a diverse array of cellular processes including growth, proliferation, differentiation and death through the protein-DNA and protein-protein interactions (for reviews, see Reeves and Beckerbauer (2001) *Biochim. Biophys. Acta* 1519: 13-29; and Reeves (2001) Gene 277: 63-81). It has been shown that HMGA proteins specifically interact with a large number of other proteins, most of which are transcription factors (Reeves (2001) *supra*). They are also subject to many types of post-translational modification. One example is phosphorylation, which markedly influences their ability to interact with DNA substrates, other proteins, and chromatin (Onate et al. (1994) *Mol. Cell Biol.* 14: 3376-3391; Falvo et al. (1995) *Cell* 83: 1101-1111; Reeves and Nissen (1995) *supra*; Huth et al. (1997) *Nat. Struct. Biol.* 4, 657-665; and Girard et al. (1998) *EMBO J.* 17: 2079-2085).

Please replace Table 1 at page 28, line 12 through page 29, line 2 with the following amended Table 1:
Table 1. ~~Gene families and binding domains~~ <u>Conserved domains and domain coordinates with the G1073 clade</u>

~~SEQ ID NO:~~	~~GID No.~~ <u>Transcription factor sequence</u>	<u>First</u> (AT-hook) and Second Conserved Domains in AA Coordinates and Base Coordinates	First domain	% ID to First Domain of G1073	Second Conserved Domain	% ID to Second Conserved Domain of G1073
[[2]]	<u>SEQ ID NO: 2:</u> G1073 AtHRC1	Polypeptide coordinates: 34-42; 78-175 Polynucleotide coordinates: 161-187; 293-586	<u>SEQ ID NO: 82:</u> RRPRGRPAG	100%	<u>SEQ ID NO: 86:</u> VSTYATRRGCGVCIISGTGAVTNVTIRQPAAPAGGGVITLHGRFDILSLTGTALPPPAPPGAGGLTVYLAGGQGQVVGGNVAGSLIASGPVVLMAASF	100%
[[4]]	<u>SEQ ID NO: 4:</u> G1067 AtHRC2	Polypeptide coordinates: 86-94, 130-235 Polynucleotide coordinates: 691-717; 823-1137	<u>SEQ ID NO: 83:</u> KRPRGRPPG	78%	<u>SEQ ID NO: 87:</u> VSTYARRRGRGVSVLGGNGTVSNVTLRQPVTPGNGGGVSGGGGVVTLHGRFEILSLTGTVLPPPAPPGAGGLSIFLAGGQGQVVGGSVVAPLIASAPVILMAASF	69%
[[6]]	<u>SEQ ID NO: 6:</u> G2153 AtHRC3	Polypeptide coordinates: 80-88, 124-227	<u>SEQ ID NO: 82:</u> RRPRGRPAG	89%	<u>SEQ ID NO: 88:</u> LATFARRRQRGICILSGNGTVANVTLRQPSTAAVA	62%

		Polynucleotide coordinates: 480-506; 612-923			AAPGGAAVLALQGRFEI LSLTGSFLPGPAPPGSTG LTIYLAGGQGQVVGGSV VGPLMAAGPVMLIAATF	
[[8]]	SEQ ID NO: 8: G2156 AtHRC4	Polypeptide coordinates: 72-80, 116-220	SEQ ID NO: 83: KRPRGRPPG	78%	SEQ ID NO: 89: VTTYARRRGRGVSILSG NGTVANVSLRQPATTAA HGANGGTGGVVALHGR FEILSLTGTVLPPPAPPGS GGLSIFLSGVQGQVIGG NVVAPLVASGPVILMAA SF	65%
[[10]]	SEQ ID NO: 10: G3399	Polypeptide coordinates: 99-107, 143-240:	SEQ ID NO: 84: RRPRGRPPG	78%	SEQ ID NO: 90: VAEYARRRGRGVCVLS GGGAVVNVALRQPGAS PPGSMVATLRGRFEILSL TGTVLPPPAPPGASGLT VFLSGGQGQVIGGSVVG PLVAAGPVVLMAAS	71%
[[12]]	SEQ ID NO: 12: G3407	Polypeptide coordinates: 63-71, 106-208	SEQ ID NO: 84: RRPRGRPPG	78%	SEQ ID NO: 91: LTAYARRRQRGVCVLSA AGTVANVTLRQPQSAQP GPASPAVATLHGRFEILS LAGSFLPPPAPPGATSLA AFLAGGQGQVVGGSVA GALIAAGPVVVVAASF	63%
[[14]]	SEQ ID NO: 14: G3456	Polypeptide coordinates: 62-70, 106-201	SEQ ID NO: 84: RRPRGRPPG	78%	SEQ ID NO: 92: VAQFARRRQRGVSILSG SGTVVNVNLRQPTAPGA VMALHGRFDILSLTGSF LPGPSPPGATGLTIYLAG GQGQIVGGEVVGPLVA AGPVLVMAATF	65%
[[16]]	SEQ ID NO: 16: G3459	Polypeptide coordinates: 76-84, 121-216	SEQ ID NO: 84: RRPRGRPPG	89%	SEQ ID NO: 93: VTAYARRRQRGICVLSG SGTVTNVSLRQPAAAGA VVTLHGRFEILSLSGSFL PPPAPPGATSLTIYLAGG QGQVVGGNVIGELTAA GPVIVIAASF	68%
[[18]]	SEQ ID NO: 18: G3460	Polypeptide coordinates: 74-82, 118-213	SEQ ID NO: 85: RRPRGRPSG	89%	SEQ ID NO: 94: VTAYARRRQRGICVLSG SGTVTNVSLRQPAAAGA VVRLHGRFEILSLSGSFL PPPAPPGATSLTIYLAGG QGQVVGGNVVGELTAA GPVIVIAASF	67%

Please replace the entire paragraph at page 96, lines 19-29 with the following amended paragraph:

The "one-hybrid" strategy (Li and Herskowitz (1993) *Science* 262: 1870-1874) is used to screen for plant cDNA clones encoding a polypeptide comprising a transcription factor DNA binding domain, a conserved domain. In brief, yeast strains are constructed that contain a lacZ reporter gene with either wild-type or mutant transcription factor binding promoter element sequences in place of the normal UAS (upstream activator sequence) of the ~~GALL~~ GAL4 promoter. Yeast reporter strains are constructed that carry transcription factor binding promoter element sequences as UAS elements are operably linked upstream (5') of a lacZ reporter gene with a minimal ~~GAL1~~ GAL4 promoter. The strains are transformed with a plant expression library that contains random cDNA inserts fused to the GAL4 activation domain (GAL4-ACT) and screened for blue colony formation on X-gal-treated filters (X-gal: 5-bromo-4-chloro-3-indolyl-β-D-galactoside; Invitrogen Corporation, Carlsbad CA). Alternatively, the strains are transformed with a cDNA polynucleotide encoding a known transcription factor DNA binding domain polypeptide sequence.

Please replace the entire paragraph at page 96, line 30 through page 97, line 4 with the following amended paragraph:

Yeast strains carrying these reporter constructs produce low levels of beta-galactosidase and form white colonies on filters containing X-gal. The reporter strains carrying wild-type transcription factor binding promoter element sequences are transformed with a polynucleotide that encodes a polypeptide comprising a plant transcription factor DNA binding domain operably linked to the acidic activator domain of the yeast GAL4 transcription factor, "GAL4-ACT". The clones that contain a polynucleotide encoding a transcription factor DNA binding domain operably linked to ~~GLA4-ACT~~ GAL4-ACT can bind upstream of the lacZ reporter genes carrying the wild-type transcription factor binding promoter element sequence, activate transcription of the lacZ gene and result in yeast forming blue colonies on X-gal-treated filters.

Please replace the prior filed Sequence Listing (MBI-0034CIP.ST25.txt filed on September 23, 2003) with the Substitute Sequence Listing "MBI-0034CIPsubs.ST25.txt", created on May 26, 2006, enclosed herewith.